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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/434,382

DATE: 11/17/1999
TIME: 13:52:25

Input Set: I434382.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

ENTERED

1 <110> APPLICANT: Tavtigian, Sean V.
2 Teng, David H.F.
3 Simard, Jacques
4 Rommens, Johanna M.
5 Myriad Genetics, Inc.
6 <120> TITLE OF INVENTION: Chromosome 17q-Linked Prostate Cancer Susceptibility
7 Gene
8 <130> FILE REFERENCE: HPC2 Gene
9 <140> CURRENT APPLICATION NUMBER: US/09/434,382
10 <141> CURRENT FILING DATE: 1999-11-05
11 <150> EARLIER APPLICATION NUMBER: US 60/107,468
12 <151> EARLIER FILING DATE: 1999-11-06
13 <160> NUMBER OF SEQ ID NOS: 213
14 <170> SOFTWARE: PatentIn Ver. 2.0
15 <210> SEQ ID NO 1
16 <211> LENGTH: 2481
17 <212> TYPE: DNA
18 <213> ORGANISM: Homo sapiens
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20 <221> NAME/KEY: CDS
21 <222> LOCATION: (1)..(2478)
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25 1 5 10 15
26 tgc cag gga cgc acc ata tgc cag gca ccc gcc cgc cgc gag cgg ccg 96
27 Ser Gln Gly Arg Thr Ile Ser Gln Ala Pro Ala Arg Arg Glu Arg Pro
28 20 25 30
29 cgc aag gac ccg ctg cgg cac ctg cgc acg cga gag aag cgc gga ccg 144
30 Arg Lys Asp Pro Leu Arg His Leu Arg Thr Arg Glu Lys Arg Gly Pro
31 35 40 45
32 tgc ggg tgc tcc ggc ggc cca aac acc gtg tac ctg cag gtg gtg gca 192
33 Ser Gly Cys Ser Gly Gly Pro Asn Thr Val Tyr Leu Gln Val Val Ala
34 50 55 60
35 gcg ggt agc cgg gac tgc ggc gcc gcg ctc tac gtc ttc tcc gag ttc 240
36 Ala Gly Ser Arg Asp Ser Gly Ala Ala Leu Tyr Val Phe Ser Glu Phe
37 65 70 75 80
38 aac cgg tat ctc ttc aac tgt gga gaa ggc gtt cag aga ctc atg cag 288
39 Asn Arg Tyr Leu Phe Asn Cys Gly Glu Gly Val Gln Arg Leu Met Gln
40 85 90 95
41 gag cac aag tta aag gtt gct cgc ctg gac aac ata ttc ctg aca cga 336
42 Glu His Lys Leu Lys Val Ala Arg Leu Asp Asn Ile Phe Leu Thr Arg
43 100 105 110
44 atg cac tgg tct aat gtt ggg ggc tta agt gga atg att ctt act tta 384

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45	Met His Trp Ser Asn Val Gly Gly Leu Ser Gly Met Ile Leu Thr Leu	
46	115 120 125	
47	aag gaa acc ggg ctt cca aag tgt gta ctt tct gga cct cca caa ctg	432
48	Lys Glu Thr Gly Leu Pro Lys Cys Val Leu Ser Gly Pro Pro Gln Leu	
49	130 135 140	
50	gaa aaa tac ctc gaa gca atc aaa ata ttt tct ggt cca ttg aaa gga	480
51	Glu Lys Tyr Leu Glu Ala Ile Lys Ile Phe Ser Gly Pro Leu Lys Gly	
52	145 150 155 160	
53	ata gaa ctg gct gtg cgg ccc cac tct gcc cca gaa tac gag gat gaa	528
54	Ile Glu Leu Ala Val Arg Pro His Ser Ala Pro Glu Tyr Glu Asp Glu	
55	165 170 175	
56	acc atg aca gtt tac cag atc ccc ata cac agt gaa cag agg agg gga	576
57	Thr Met Thr Val Tyr Gln Ile Pro Ile His Ser Glu Gln Arg Arg Gly	
58	180 185 190	
59	aag cac caa cca tgg cag agt cca gaa agg cct ctc agc agg ctc agt	624
60	Lys His Gln Pro Trp Gln Ser Pro Glu Arg Pro Leu Ser Arg Leu Ser	
61	195 200 205	
62	cca gag cga tct tca gac tcc gag tcg aat gaa aat gag cca cac ctt	672
63	Pro Glu Arg Ser Ser Asp Ser Glu Ser Asn Glu Asn Glu Pro His Leu	
64	210 215 220	
65	cca cat ggt gtt agc cag aga aga ggg gtc agg gac tct tcc ctg gtc	720
66	Pro His Gly Val Ser Gln Arg Arg Gly Val Arg Asp Ser Ser Leu Val	
67	225 230 235 240	
68	gta gct ttc atc tgt aag ctt cac tta aag aga gga aac ttc ttg gtg	768
69	Val Ala Phe Ile Cys Lys Leu His Leu Lys Arg Gly Asn Phe Leu Val	
70	245 250 255	
71	ctc aaa gca aag gag atg ggc ctc cca gtt ggg aca gct gcc atc gct	816
72	Leu Lys Ala Lys Glu Met Gly Leu Pro Val Gly Thr Ala Ala Ile Ala	
73	260 265 270	
74	ccc atc att gct gct gtc aag gac ggg aaa agc atc act cat gaa gga	864
75	Pro Ile Ile Ala Ala Val Lys Asp Gly Lys Ser Ile Thr His Glu Gly	
76	275 280 285	
77	aga gag att ttg gct gaa gag ctg tgt act cct cca gat cct ggt gct	912
78	Arg Glu Ile Leu Ala Glu Glu Leu Cys Thr Pro Pro Asp Pro Gly Ala	
79	290 295 300	
80	gct ttt gtg gtg gta gaa tgt cca gat gaa agc ttc att caa ccc atc	960
81	Ala Phe Val Val Val Glu Cys Pro Asp Glu Ser Phe Ile Gln Pro Ile	
82	305 310 315 320	
83	tgt gag aat gcc acc ttt cag agg tac caa gga aag gca gat gcc ccc	1008
84	Cys Glu Asn Ala Thr Phe Gln Arg Tyr Gln Gly Lys Ala Asp Ala Pro	
85	325 330 335	
86	gtg gcc ttg gtg gtt cac atg gcc cca gca tct gtg ctt gtg gac agc	1056
87	Val Ala Leu Val Val His Met Ala Pro Ala Ser Val Leu Val Asp Ser	
88	340 345 350	
89	agg tac cag cag tgg atg gag agg ttt ggg cct gac acc cag cac ttg	1104
90	Arg Tyr Gln Gln Trp Met Glu Arg Phe Gly Pro Asp Thr Gln His Leu	
91	355 360 365	
92	gtc ctg aat gag aac tgt gcc tca gtt cac aac ctt cgc agc cac aag	1152
93	Val Leu Asn Glu Asn Cys Ala Ser Val His Asn Leu Arg Ser His Lys	
94	370 375 380	

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95	att caa acc cag ctc aac ctc atc cac ccg gac atc ttc ccc ctg ctc	1200
96	Ile Gln Thr Gln Leu Asn Leu Ile His Pro Asp Ile Phe Pro Leu Leu	
97	385 390 395 400	
98	acc agt ttc cgc tgt aag aag gag ggc ccc acc ctc agt gtg ccc atg	1248
99	Thr Ser Phe Arg Cys Lys Lys Glu Gly Pro Thr Leu Ser Val Pro Met	
100	405 410 415	
101	gtt cag ggt gaa tgc ctc ctc aag tac cag ctc cgt ccc agg agg gag	1296
102	Val Gln Gly Glu Cys Leu Leu Lys Tyr Gln Leu Arg Pro Arg Arg Glu	
103	420 425 430	
104	tgg cag agg gat gcc att att act tgc aat cct gag gaa ttc ata gtt	1344
105	Trp Gln Arg Asp Ala Ile Ile Thr Cys Asn Pro Glu Glu Phe Ile Val	
106	435 440 445	
107	gag gcg ctg cag ctt ccc aac ttc cag cag agc gtg cag gag tac agg	1392
108	Glu Ala Leu Gln Leu Pro Asn Phe Gln Gln Ser Val Gln Glu Tyr Arg	
109	450 455 460	
110	agg agt gcg cag gac ggc cca gcc cca gca gag aaa aga agt cag tac	1440
111	Arg Ser Ala Gln Asp Gly Pro Ala Pro Ala Glu Lys Arg Ser Gln Tyr	
112	465 470 475 480	
113	cca gaa atc atc ttc ctt gga aca ggg tct gcc atc ccg atg aag att	1488
114	Pro Glu Ile Ile Phe Leu Gly Thr Gly Ser Ala Ile Pro Met Lys Ile	
115	485 490 495	
116	cga aat gtc agt gcc aca ctt gtc aac ata agc ccc gac acg tct ctg	1536
117	Arg Asn Val Ser Ala Thr Leu Val Asn Ile Ser Pro Asp Thr Ser Leu	
118	500 505 510	
119	cta ctg gac tgt ggt gag ggc aca ttt ggg cag ctg tgc cgt cat tac	1584
120	Leu Leu Asp Cys Gly Glu Gly Thr Phe Gly Gln Leu Cys Arg His Tyr	
121	515 520 525	
122	gga gac cag gtg gac agg gtc ctg ggc acc ctg gct gct gtg ttt gtg	1632
123	Gly Asp Gln Val Asp Arg Val Leu Gly Thr Leu Ala Ala Val Phe Val	
124	530 535 540	
125	tcc cac ctg cac gca gat cac cac acg ggc ttg cca agt atc ttg ctg	1680
126	Ser His Leu His Ala Asp His His Thr Gly Leu Pro Ser Ile Leu Leu	
127	545 550 555 560	
128	cag aga gaa cgc gcc ttg gca tct ttg gga aag ccg ctt cac cct ttg	1728
129	Gln Arg Glu Arg Ala Leu Ala Ser Leu Gly Lys Pro Leu His Pro Leu	
130	565 570 575	
131	ctg gtg gtt gcc ccc aac cag ctc aaa gcc ttg ctc cag cag tac cac	1776
132	Leu Val Val Ala Pro Asn Gln Leu Lys Ala Trp Leu Gln Gln Tyr His	
133	580 585 590	
134	aac cag tgc cag gag gtc ctg cac cac atc agt atg att cct gcc aaa	1824
135	Asn Gln Cys Gln Glu Val Leu His His Ile Ser Met Ile Pro Ala Lys	
136	595 600 605	
137	tgc ctt cag gaa ggg gct gag atc tcc agt cct gca gtg gaa aga ttg	1872
138	Cys Leu Gln Glu Gly Ala Glu Ile Ser Ser Pro Ala Val Glu Arg Leu	
139	610 615 620	
140	atc agt tcg ctg ttg cga aca tgt gat ttg gaa gag ttt cag acc tgt	1920
141	Ile Ser Ser Leu Leu Arg Thr Cys Asp Leu Glu Glu Phe Gln Thr Cys	
142	625 630 635 640	
143	ctg gtg cgg cac tgc aag cat gcg ttt ggc tgt gcg ctg gtg cac acc	1968
144	Leu Val Arg His Cys Lys His Ala Phe Gly Cys Ala Leu Val His Thr	

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145				645				650				655					
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147	Ser	Gly	Trp	Lys	Val	Val	Tyr	Ser	Gly	Asp	Thr	Met	Pro	Cys	Glu	Ala	
148				660				665					670				
149	ctg	gtc	cgg	atg	ggg	aaa	gat	gcc	acc	ctc	ctg	ata	cat	gaa	gcc	acc	2064
150	Leu	Val	Arg	Met	Gly	Lys	Asp	Ala	Thr	Leu	Leu	Ile	His	Glu	Ala	Thr	
151				675				680					685				
152	ctg	gaa	gat	ggt	ttg	gaa	gag	gaa	gca	gtg	gaa	aag	aca	cac	agc	aca	2112
153	Leu	Glu	Asp	Gly	Leu	Glu	Glu	Glu	Ala	Val	Glu	Lys	Thr	His	Ser	Thr	
154				690				695					700				
155	acg	tcc	caa	gcc	atc	agc	gtg	ggg	atg	cgg	atg	aac	gcg	gag	ttc	att	2160
156	Thr	Ser	Gln	Ala	Ile	Ser	Val	Gly	Met	Arg	Met	Asn	Ala	Glu	Phe	Ile	
157																	
158	atg	ctg	aac	cac	ttc	agc	cag	cg	tat	gcc	aag	gtc	ccc	ctc	ttc	agc	2208
159	Met	Leu	Asn	His	Phe	Ser	Gln	Arg	Tyr	Ala	Lys	Val	Pro	Leu	Phe	Ser	
160					725					730				735			
161	ccc	aac	ttc	agc	gag	aaa	gtg	gga	gtt	gcc	ttt	gac	cac	atg	aag	gtc	2256
162	Pro	Asn	Phe	Ser	Glu	Lys	Val	Gly	Val	Ala	Phe	Asp	His	Met	Lys	Val	
163					740					745				750			
164	tg	ttt	gga	gac	ttt	cca	aca	atg	ccc	aag	ctg	att	ccc	cca	ctg	aaa	2304
165	Cys	Phe	Gly	Asp	Phe	Pro	Thr	Met	Pro	Lys	Leu	Ile	Pro	Pro	Leu	Lys	
166					755					760				765			
167	gcc	ctg	ttt	gct	ggc	gac	atc	gag	gag	atg	gag	gag	cg	agg	gag	aag	2352
168	Ala	Leu	Phe	Ala	Gly	Asp	Ile	Glu	Glu	Met	Glu	Glu	Arg	Arg	Glu	Lys	
169					770					775				780			
170	cgg	gag	ctg	cgg	cag	gtg	cgg	gcg	gcc	ctc	ctg	tcc	agg	gag	ctg	gca	2400
171	Arg	Glu	Leu	Arg	Gln	Val	Arg	Ala	Ala	Leu	Leu	Ser	Arg	Glu	Leu	Ala	
172																	
173	ggc	ggc	ctg	gag	gat	ggg	gag	cct	cag	cag	aag	cgg	gcc	cac	aca	gag	2448
174	Gly	Gly	Leu	Glu	Asp	Gly	Glu	Pro	Gln	Gln	Lys	Arg	Ala	His	Thr	Glu	
175					805					810				815			
176	gag	cca	cag	gcc	aag	aag	gtc	aga	gcc	cag	tga						2481
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187					20					25				30			
188	Arg	Lys	Asp	Pro	Leu	Arg	His	Leu	Arg	Thr	Arg	Glu	Lys	Arg	Gly	Pro	
189					35					40				45			
190	Ser	Gly	Cys	Ser	Gly	Gly	Pro	Asn	Thr	Val	Tyr	Leu	Gln	Val	Val	Ala	
191					50					55				60			
192	Ala	Gly	Ser	Arg	Asp	Ser	Gly	Ala	Ala	Leu	Tyr	Val	Phe	Ser	Glu	Phe	
193					65					70				75		80	
194	Asn	Arg	Tyr	Leu	Phe	Asn	Cys	Gly	Glu	Gly	Val	Gln	Arg	Leu	Met	Gln	

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195				85				90				95				
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198	Met	His	Trp	Ser	Asn	Val	Gly	Gly	Leu	Ser	Gly	Met	Ile	Leu	Thr	Leu
199			115					120				125				
200	Lys	Glu	Thr	Gly	Leu	Pro	Lys	Cys	Val	Leu	Ser	Gly	Pro	Pro	Gln	Leu
201		130					135				140					
202	Glu	Lys	Tyr	Leu	Glu	Ala	Ile	Lys	Ile	Phe	Ser	Gly	Pro	Leu	Lys	Gly
203	145				150					155					160	
204	Ile	Glu	Leu	Ala	Val	Arg	Pro	His	Ser	Ala	Pro	Glu	Tyr	Glu	Asp	Glu
205				165					170			175				
206	Thr	Met	Thr	Val	Tyr	Gln	Ile	Pro	Ile	His	Ser	Glu	Gln	Arg	Arg	Gly
207			180					185				190				
208	Lys	His	Gln	Pro	Trp	Gln	Ser	Pro	Glu	Arg	Pro	Leu	Ser	Arg	Leu	Ser
209		195					200				205					
210	Pro	Glu	Arg	Ser	Ser	Asp	Ser	Glu	Ser	Asn	Glu	Asn	Glu	Pro	His	Leu
211		210				215				220						
212	Pro	His	Gly	Val	Ser	Gln	Arg	Arg	Gly	Val	Arg	Asp	Ser	Ser	Leu	Val
213	225				230				235						240	
214	Val	Ala	Phe	Ile	Cys	Lys	Leu	His	Leu	Lys	Arg	Gly	Asn	Phe	Leu	Val
215				245				250				255				
216	Leu	Lys	Ala	Lys	Glu	Met	Gly	Leu	Pro	Val	Gly	Thr	Ala	Ala	Ile	Ala
217			260				265				270					
218	Pro	Ile	Ile	Ala	Ala	Val	Lys	Asp	Gly	Lys	Ser	Ile	Thr	His	Glu	Gly
219		275				280					285					
220	Arg	Glu	Ile	Leu	Ala	Glu	Glu	Leu	Cys	Thr	Pro	Pro	Asp	Pro	Gly	Ala
221		290				295				300						
222	Ala	Phe	Val	Val	Val	Glu	Cys	Pro	Asp	Glu	Ser	Phe	Ile	Gln	Pro	Ile
223	305				310				315						320	
224	Cys	Glu	Asn	Ala	Thr	Phe	Gln	Arg	Tyr	Gln	Gly	Lys	Ala	Asp	Ala	Pro
225				325				330				335				
226	Val	Ala	Leu	Val	Val	His	Met	Ala	Pro	Ala	Ser	Val	Leu	Val	Asp	Ser
227			340				345				350					
228	Arg	Tyr	Gln	Gln	Trp	Met	Glu	Arg	Phe	Gly	Pro	Asp	Thr	Gln	His	Leu
229		355				360					365					
230	Val	Leu	Asn	Glu	Asn	Cys	Ala	Ser	Val	His	Asn	Leu	Arg	Ser	His	Lys
231		370				375				380						
232	Ile	Gln	Thr	Gln	Leu	Asn	Leu	Ile	His	Pro	Asp	Ile	Phe	Pro	Leu	Leu
233	385				390				395						400	
234	Thr	Ser	Phe	Arg	Cys	Lys	Lys	Glu	Gly	Pro	Thr	Leu	Ser	Val	Pro	Met
235				405				410				415				
236	Val	Gln	Gly	Glu	Cys	Leu	Leu	Lys	Tyr	Gln	Leu	Arg	Pro	Arg	Arg	Glu
237			420					425				430				
238	Trp	Gln	Arg	Asp	Ala	Ile	Ile	Thr	Cys	Asn	Pro	Glu	Glu	Phe	Ile	Val
239		435					440				445					
240	Glu	Ala	Leu	Gln	Leu	Pro	Asn	Phe	Gln	Gln	Ser	Val	Gln	Glu	Tyr	Arg
241		450				455				460						
242	Arg	Ser	Ala	Gln	Asp	Gly	Pro	Ala	Pro	Ala	Glu	Lys	Arg	Ser	Gln	Tyr
243	465				470				475			480				
244	Pro	Glu	Ile	Ile	Phe	Leu	Gly	Thr	Gly	Ser	Ala	Ile	Pro	Met	Lys	Ile

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.



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VERIFICATION SUMMARY
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DATE: 11/17/1999
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Line	? Error/Warning	Original Text
877	W "N" or "Xaa" used: Feature required	agcatcactc atgaaggaag agaggtgaga tgcctggt
1109	W "N" or "Xaa" used: Feature required	caggaattca gcacatactc attgttcagn n
1331	W "N" or "Xaa" used: Feature required	caggaattca gcacatactc attgttcagn n